



## SEQUENCE LISTING

<110> Sun, Lee-Hwei K  
Sun, Bill N  
Sun, Cecily R

<120> Fc fusion proteins of human erythropoietin with increased biological activities

<130> 02SUN2001

<140> 09/932812

<141> 2001-08-17

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

cccaagcttg gcgcggagat gggggtgca  
29

<210> 2

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 2

cggatccgctc ccctgtcctg caggcct  
27

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 3

gagcgcaaat gttgtgtcga  
20

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 4

ggaattctca tttacccgga gacaggga  
28

<210> 5

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 5

tggttttctc gatggaggct gggaggcct  
29

<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 6

aggcctccca gcctccatcg agaaaacca  
29

cb  
cont

<210> 7  
<211> 69  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 7  
cggatccggt ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agcgcaaag  
60

ttgtgtcga  
69

<210> 8  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 8  
gagtcctaat atggtcccc a  
21

<210> 9  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 9  
ggaattctca ttaccacaga gacaggga  
28

<210> 10  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 10  
cctgagttcg cggggggacc a  
21

<210> 11  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 11  
gagtccaaat atggtccccc atgccaccca tgcccagcac ctgagttcgc ggggggacca  
60

<210> 12  
<211> 70  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 12  
cggatccggt ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agtccaaata  
60

tggtccccc  
70

<210> 13  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 13  
gacaaaactc acacatgccc a  
21

<210> 14  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 14  
acctgaagtc gcgggggggac cgt  
23

<210> 15  
<211> 55  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 15  
gacaaaactc acacatgccc accgtgcccga gcacctgaag tcgcggggggg accgt  
55

<210> 16  
<211> 70  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 16  
cggatccggt ggcggttccg gtggaggcgg aagcggcggt ggaggatcag acaaaaactca  
60

cacatgcccga  
70

<210> 17  
<211> 1332  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; HuEPO-L-vFc gamma2 (Figure 2A)

&lt;400&gt; 17

aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc  
60

ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac  
120

agccgagtcc tggagaggta cctcttggag gccaaggagg ccgagaatat caccacgggc  
180

tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc  
240

tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc  
300

ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg  
360

gagcccctgc agctgcatgt ggataaagcc gtcagtggcc ttgcagcct caccactctg  
420

cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagtgtct  
480

ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc  
540

ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt  
600

ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agcgcaaata ttgtgtcgag  
660

tgcccaccgt gcccagcacc acctgtggca ggaccgtcag tcttcctctt cccccaaaa  
720

cccaaggaca ccctcatgat ctcccggacc cctgagggtca cgtgcgtggg ggtggacgtg  
780

agccacgaag accccgaggt ccagttcaac tggtagctgg acggcgtgga ggtgcataat  
840

gccaaagaaa agccacggga ggagcagttc aacagcacgt tccgtgtggg cagcgtcctc  
900

accgttgtgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa  
960

ggcctcccag cctccatcga gaaaaccatc tccaaaacca aagggcagcc ccgagaacca  
1020

caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc  
1080

tgcctgggtca aaggcttcta cccagcgcac atcgccgtgg agtgggagag caatgggcag  
1140

ccggagaaca actacaagac cacacctccc atgctggact ccgacggctc cttcttcttc  
1200

tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcattgctcc  
1260

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt  
1320

aaatgagaat tc  
1332

<210> 18

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2 A)

<400> 18

Met	Gly	Val	His	Glu	Cys	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Leu	Ser	Leu
1				5					10					15	

Leu	Ser	Leu	Pro	Leu	Gly	Leu	Pro	Val	Leu	Gly	Ala	Pro	Pro	Arg	Leu
			20					25						30	

Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu
		35					40					45			

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu  
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu  
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser  
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly  
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu  
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile  
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu  
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
 180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 195 200 205

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val  
 210 215 220

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 225 230 235 240



Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
420 425 430

Ser Pro Gly Lys  
435

<210> 19  
<211> 1335  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> HuEPO-L-vFc gamma4 (Figure 2B)

<400> 19  
aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc  
60  
  
ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac  
120  
  
agccgagtcc tggagaggta cctcttggag gccaggagg ccgagaatat caccacgggc  
180  
  
tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc  
240  
  
tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc  
300  
  
ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg  
360  
  
gagccctgc agctgcatgt ggataaagcc gtcagtggcc ttgcagcct caccactctg  
420  
  
cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct  
480  
  
ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc  
540  
  
ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt  
600  
  
ggcgggtccg gtggaggcgg aagcggcggt ggaggatcag agtccaaata tgggtcccca  
660

tgcccacccat gccagcacc tgagttcgcg gggggacccat cagtcttcct gttcccccca  
720

aaacccaagg acactctcat gatctcccg acccctgagg tcacgtgcgt ggtggtggac  
780

gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat  
840

aatgccaaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc  
900

ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac  
960

aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag  
1020

ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg  
1080

acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg  
1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctctttcttc  
1200

ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc  
1260

tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctctg  
1320

ggtaaatgag aattc  
1335

<210> 20

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure 2B)  
)

<400> 20

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu  
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu  
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu  
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu  
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu  
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser  
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly  
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu  
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile  
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu  
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
 180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 195 200 205

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe  
 210 215 220

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 225 230 235 240

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 245 250 255

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val  
 260 265 270

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser  
 275 280 285

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 290 295 300

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser  
 305 310 315 320

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 325 330 335

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln  
 340 345 350

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 355 360 365

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 370 375 380

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu  
 385 390 395 400

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser  
 405 410 415

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 420 425 430

Leu Ser Leu Gly Lys  
 435

<210> 21  
 <211> 1329  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HuEPO-L-vFc gamma1 (Figure 2C)

<400> 21  
 aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc  
 60

ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac  
 120

agccgagtcc tggagaggta cctcttggag gccaaaggagg ccgagaatat caccacgggc  
 180

tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc  
 240

tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc  
 300

ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg  
 360

gagccctgc agctgcatgt ggataaagcc gtcagtggcc ttgcagcct caccactctg  
 420

cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct

480

ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc  
540

ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt  
600

ggcggttccg gtggaggcgg aagcggcggg ggaggatcag acaaaaactca cacatgccca  
660

ccgtgcccag cacctgaagt cgcgggggga ccgtcagtct tcctcttccc cccaaaaccc  
720

aaggacaccc tcatgatctc ccggacacct gaggtcacat gcgtggtggt ggacgtgagc  
780

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc  
840

aagacaaagc cgcgggagga gcagtacaac agcacgtacc ggggtggtcag cgtcctcacc  
900

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggctct caacaaagcc  
960

ctcccagcct ccacgcagaa aaccatctcc aaagccaaag ggcagccccc agaaccacag  
1020

gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc  
1080

ctgggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg  
1140

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac  
1200

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg  
1260

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa  
1320

tgagaattc  
1329

<210> 22  
 <211> 435  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HuEPO-L-vFc gamma1 with a 27-amino acid leader peptide (Figure 2C)  
 )

<400> 22

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu  
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu  
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu  
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu  
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu  
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser  
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly  
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu  
 130 135 140



Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile  
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu  
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
 180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 195 200 205

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Val Ala Gly  
 210 215 220

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 225 230 235 240

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 245 250 255

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 260 265 270

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 275 280 285

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 290 295 300

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile  
 305 310 315 320

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 325 330 335

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 340 345 350

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 355 360 365

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 370 375 380

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 385 390 395 400

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 405 410 415

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 420 425 430

Pro Gly Lys  
 435

<210> 23  
 <211> 16  
 <212> PRT  
 <213> Artificial sequence, 16-amino acid peptide linker

<400> 23

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5 10 15

<210> 24  
 <211> 15  
 <212> PRT  
 <213> Human IgG1 hinge sequence

<400> 24

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 1 5 10 15

<210> 25  
 <211> 10  
 <212> PRT  
 <213> Truncated human IgG1 hinge sequence  
 <400> 25

Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 1 5 10

<210> 26  
 <211> 232  
 <212> PRT  
 <213> Human IgG1 Fc with native hinge, CH2 and CH3 domains  
 <400> 26

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
 1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys  
 225 230

<210> 27

<211> 228

<212> PRT

<213> Human IgG2 Fc with native hinge, CH2 and CH3 domains

<400> 27

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val  
 1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

35	40	45
His Glu Asp Pro Glu Val	Gln Phe Asn Trp Tyr	Val Asp Gly Val Glu
50	55	60
Val His Asn Ala Lys Thr	Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr	
65	70	75
Phe Arg Val Val Ser Val Leu Thr Val	Val His Gln Asp Trp Leu Asn	
	85	90
Gly Lys Glu Tyr Lys Cys Lys Val	Ser Asn Lys Gly Leu Pro Ala Pro	
	100	105
Ile Glu Lys Thr Ile Ser Lys Thr	Lys Gly Gln Pro Arg Glu Pro Gln	
	115	120
Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met	Thr Lys Asn Gln Val	
	130	135
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr	Pro Ser Asp Ile Ala Val	
	145	150
Glu Trp Glu Ser Asn Gly Gln Pro Glu	Asn Asn Tyr Lys Thr Thr Pro	
	165	170
Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr	Ser Lys Leu Thr	
	180	185
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe	Ser Cys Ser Val	
	195	200
Met His Glu Ala Leu His Asn His Tyr Thr Gln	Lys Ser Leu Ser Leu	
	210	215
Ser Pro Gly Lys		220

225

<210> 28  
 <211> 229  
 <212> PRT  
 <213> Human IgG4 Fc with native hinge, CH2 and CH3 domains  
 <400> 28

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe  
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val  
 50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser  
 65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser  
 100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln  
 130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu  
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser  
195 200 205

C<sup>6</sup> Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
210 215 220

Leu Ser Leu Gly Lys  
225

---